MODULARITY OF 3D FACES FOR GENDER AND ANCESTRY PREDICTION

Džemila Šero[1], Mark D. Shriver[2], Dirk Vandermeulen[1], Peter Claes[1]

[1] KU Leuven, ESAT/PSI - UZ Leuven, MIRC - iMinds, Medical IT Dept. [2] Department of Anthropology, Penn State University, University Park, Pennsylvania, United States of America.

Background: Facial gender and ancestry draw the signature of human heterogeneity in terms of inter-subject distinctiveness and personal individuality. The common 3D face-based gender prediction models use families of curve features as robust representations of the facial surface [1]. A feature selection is then performed to retain the most salient curves for classification purposes. More recent work combines 3D shape-related and 2D textural features of the face [2]. The result is a novel local descriptor that together with a feature selection framework finds the most discriminative characteristics to improve the performance of gender and ethnicity prediction. We propose to investigate the 3D facial shape from a modular and thus local perspective. First, we segment the surface into patches/modules through normalized spectral clustering [3]. Second, we calculate the singular values of the Euclidean distance matrices as a compact representation of each extracted patch/module.

Aims: Provide evidence that facial gender and ancestry prediction improves with the segmentation of the 3D face into an increasing number of compact subunits.

Methods: A dataset of 592 3D faces, represented as spatially dense meshes of 7,150 corresponding quasi-landmarks and continuously ranging from European to African ancestry, is first normalized using Generalized Procrustes Alignment. We apply normalized spectral clustering to this aligned dataset, grouping vertices that are strongly spatially correlated and connected to form compact modules. Given an average mesh configuration of the whole set of faces, we first build the affinity matrix that encodes the similarity of each pair of landmarks in the following way:

$$A = \lambda * \bar{C} + (1 - \lambda) * \bar{G}, \qquad (1)$$

which assigns a high weight (λ) to strongly correlated landmark pairs ($\bar{C}$), while penalizing their inter-landmark geodesic distance ($\bar{G}$) measured on the average mesh configuration. The normalized Laplacian matrix of this affinity matrix is computed and its top-k eigenvectors are retained. The traditional K-means algorithm is used to cluster the first eigenvectors, initializing the centers with a weighted probability distribution to account for variability due to seed selection. Since the point correspondences are known, an appropriate cluster representation is the Euclidean distance matrix (EDM) between each pair of landmarks in each cluster. The S largest singular values of this EDM are computed and retained as cluster shape descriptors. The relative inter-cluster configuration is taken into account by computing the centroids of each module and calculating the top singular values of the EDM of their coordinates. The feature space is thus the concatenation of the singular values resulting from the Euclidean distance matrix of the modules and their centroids. Gender classification is performed through linear discriminant analysis (LDA), least-squares support vector machines with a linear kernel (LSSVM), and logistic regression (LR). For ancestry prediction we use partial least squares (PLSR) and multiple linear (MR) regression, and random decision forest (RDF).

Results: Increasing the number of modules leads to improved performance for all the classifiers and regressors used. After a strong initial improvement phase, performance reaches a plateau with little significant variations. Gender classification accuracies are always above 94% starting from eight clusters (Figure 1 (middle)), compared to 86.05% in [1] and 95.45% in [2]. The correlation coefficients of ancestry regression reach values above 0,75 from eleven clusters on (Figure 1 (right)).

Conclusions: The performance values, both in gender and ancestry prediction, confirm the hypothesis that investigating the 3D face from a *macro-to-micro* perspective enhances gender and ancestry predictions. Furthermore, the singular values turn out to be good shape descriptors for this goal.

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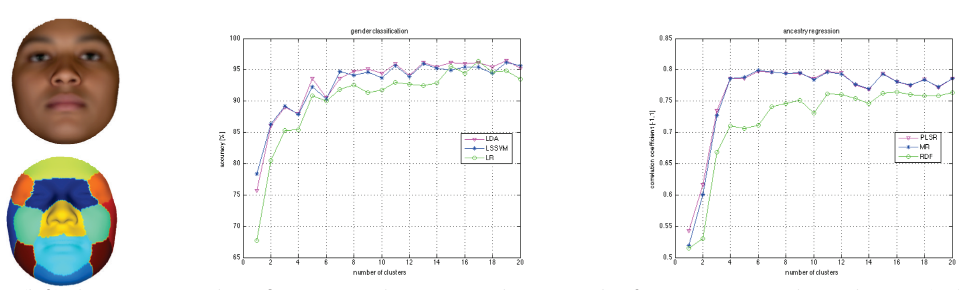

Figure 1: *(left) The average mesh configuration with texture, and an example of segmentation with ten clusters. (right) Comparative graphs for gender and ancestry prediction, respectively.*